

## Attachment

### SEQ ID NO 3: Wild-type glucanase from Teather et al, 1988.

1. 27 signal peptide sequence in the N-terminus (up-lined), which is not present in the truncated glucanase.
2. catalytic domain of glucanase (shaded) that is important and essential for the catalytic activity of the enzyme.
3. 78 residues (up-lined) are deleted in truncated glucanases (SEQ NO 1 & 2) at the C-terminus

ATGAACATCAAGAAA**ACTGCAGTCAGTCAGAGCGCTCTCGCCGTAGCAGCCG**CAGCAGCAGCC  
M N I K K T A V K S A L A V A A A A A A A 20

CTCACCAAC**ATGTTAGCGAAAGGATT**TTAGCGGTGCCA**ACTCTACACGTTAGAAGAA**  
L T T N V S A K D F S G A E L Y T L E E 40

GTTCA**GTACGGTAAGTTGAAGCCG**TATGAAGATGGCAGCCGATCGGAAC**ACTCACT**  
V Q Y G K F E A R M K M A A A S G T V S 60

TCCATGTTCT**CTACCAGAACATGGTCCGAAATCGCCATGGAAGGCCCTGGTAGAAGTG**  
S M F L Y Q N G S E I A D G R P W V E V 80

GATATTGAAG**TTCTCGGCAAGAACATCCGGCAGTTCCAGTCCAACATCATTACCGTAAG**  
D I E V L G K N P G S F Q S N I I T G K 100

GCCGGCGCACAAAG**ACTAGCGAAAGCACCATGCTGTTAGCCCCGCCGATCAGGCT**  
A G A Q K T S E K H H A V S P A A D Q A 120

TTCCACAC**CTACGGTCTCGAATGGACTCCGAATTACGTCCGCTGGACTGTTGACGGTCAG**  
F H T Y G L E W T P N Y V R W T V D G Q 140

GAAGTCCGCAAGACGGAA**AGGTGGCCAGGTTCCAAC**TTGACAGGTACACAGGGACTCCG  
E V R K T E G G Q V S N L T G T Q G L R 160

TTAACCTT**GGCTCTGAGAGTGGGGTTGGGTGCCCAGTTGATGAATCAAAGCTT**  
F N L W S S E S A A W V G Q F D E S K L 180

CCGCTT**CCAGTTCATCAACTGGGTCAAGGTTATAAGTATACGCCGGGCCAGGGCGAA**  
P L F Q F I N W V K V Y K Y T P G Q G E 200

GGCGGCA**GGCAGTTACGCTGACTGGGACACGACAATTGACACGTTGATGGCTCCGC**  
G G S D F T L D W T D N F D T F D G S R 220

TGGGGCAAGGG**TGACTGGACATTGACGGTAACCGTGTGACCTCACCGACAAGAACATC**  
W G K G D W T F D G N R V D L T D K N I 240

TACTCCAGAGATGG**CATGTTGATCCTCGCCCTACCCGAAAGGTCAAGGAAAGCTTCAAC**  
Y S R D G M L I L A L T R K G Q E S F N 260

GGCCAGGTT**CCGAGAGATGACGAACCTGCTCCGCAATCTCTAGCAGCGCTCCGGCATCT**  
G Q V P R D D E P A P Q S S S S A P A S 280

TCTAGCAGT**GTTCGGCAAGCTCCTCTAGCGTCCCTGCCCTCGAGCAGCGCATTTGTT**  
S S S V P A S S S S V P A S S S S A F V 300

CCGGCGAGCT**CTCGAGGCCACAAACCGCAATCCACCGAATGCCACAAACTCCCCAGTT**  
P P S S S S A T N A I H G M R T T P A V 320

GCAAAGGAAC**ACCCGCAATCTCGTGAACGCCAAGGGTGC**CAAGGTGAACCCGAATGGCCAC  
A K E H R N L V N A K G A K V N P N G H 340

AAGCGTTATCGCGTGAACTTGAACACTAA  
K R Y R V N F E H \*

349

**SEQ ID NO 11:**

78 residues composed of PXSSSS repeats and a basic terminal domain (BTD) (shaded) at the C-terminus of wild-type glucanase (SEQ ID: No 3 from Teather et al) are deleted in TF-glucanase (SEQ ID: No 1) and PCR-TF-glucanase (SEQ ID: No 2)

CAATCTTCTAGCAGCGCTCCGGCATCT  
Q S S S S A P A S 280

TCTAGCAGTGTCCGGCAAGCTCCTCTAGCGTCCCTGCCCTCGAGCAGGGCATTTGTT  
S S S V P A S S S S V P A S S S S A F V 300

CCGGCGAGCTCCTCGAGCGCCACAAACGCAATCCACCGAATGCGCACAACTCCGGCAGTT  
P P S S S S A T N A I H G M R T T P A V 320

GCAAAGGAACACCGCAATCTCGTGAACGCCAAGGGTCCAAGGTGAACCCGAATGGCCAC  
A K E H R N L V N A K G A K V N P N G H 340

AAGCGTTATCGCGTGAACTTGAACACTAA  
K R Y R V N F E H \*

349